

MalE-CORE+1 RECOMBINANT PROTEINS

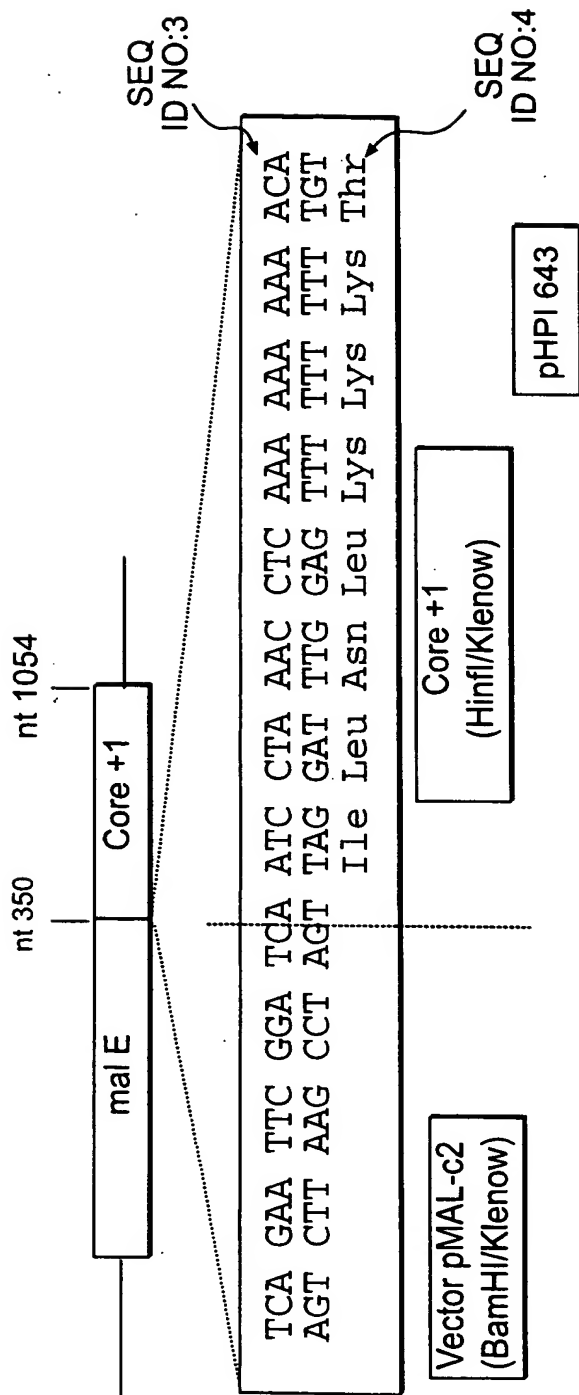


FIG. 1A



MalE-CORE+1 RECOMBINANT PROTEINS

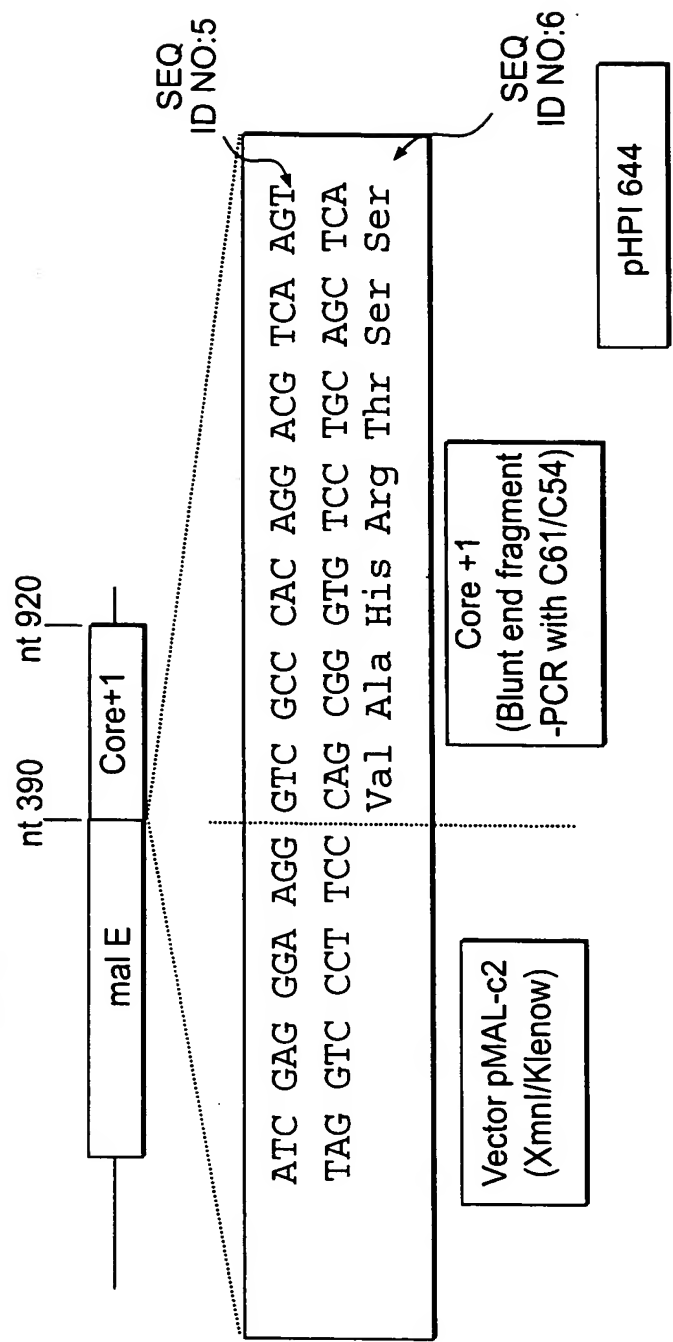


FIG. 1B

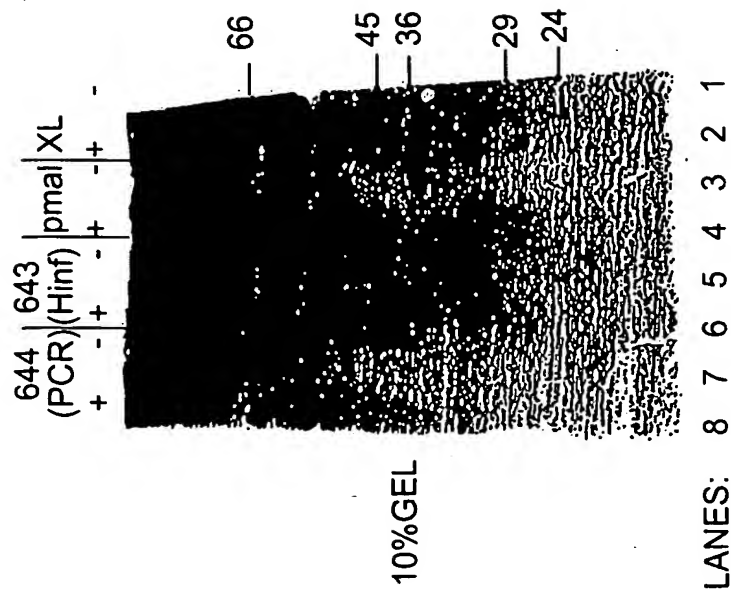


FIG. 2A

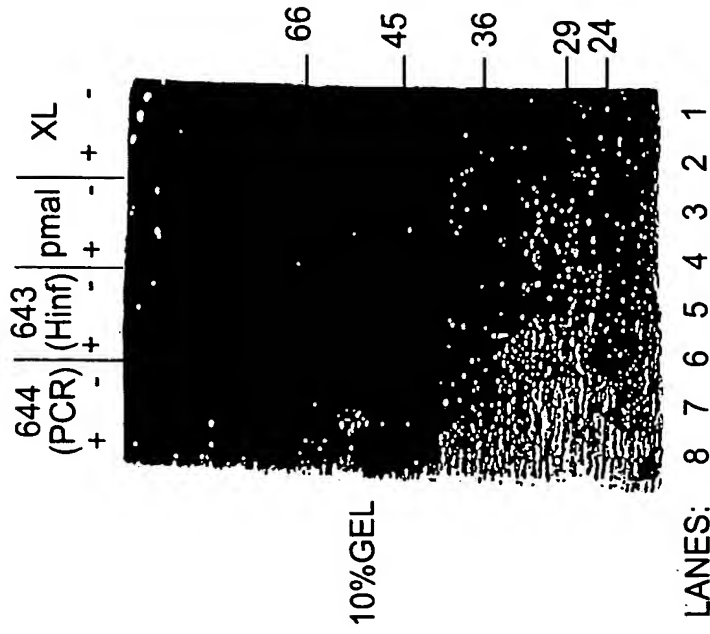


FIG. 2B

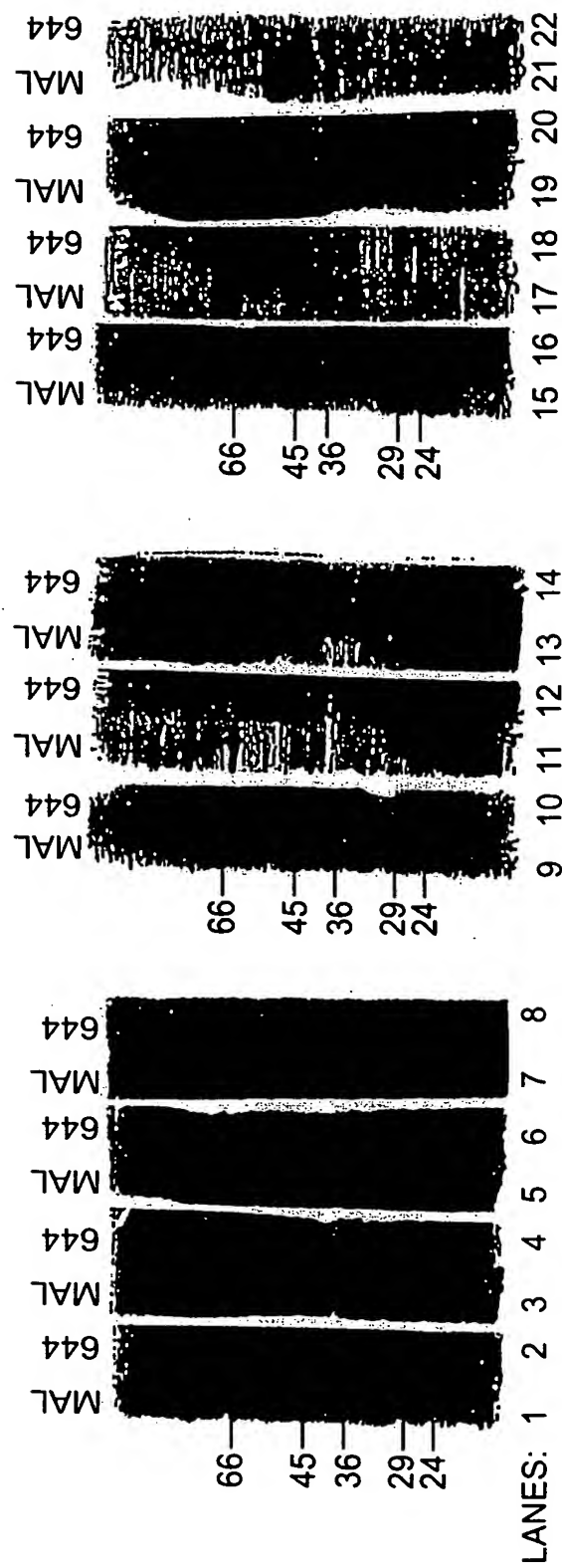


FIG. 3A

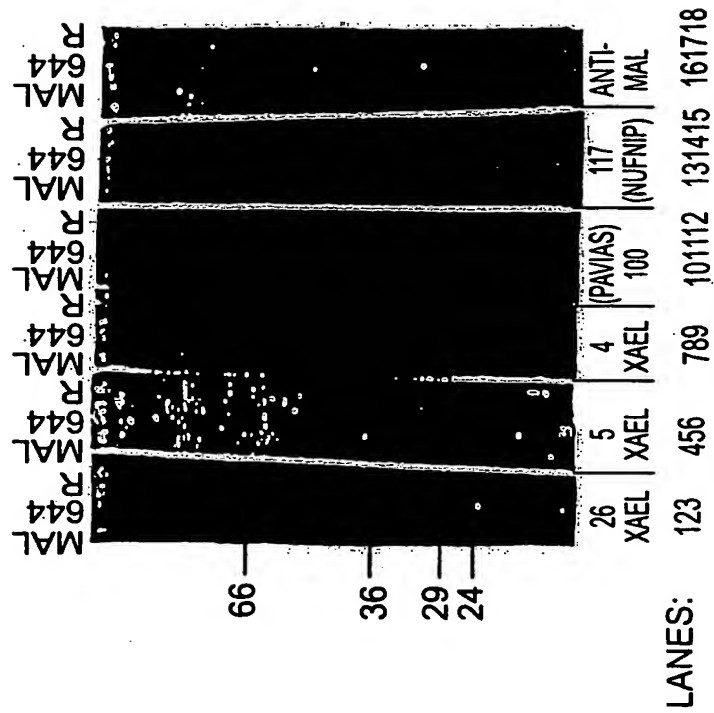


FIG. 3B

GST-CORE+1 RECOMBINANT PROTEINS

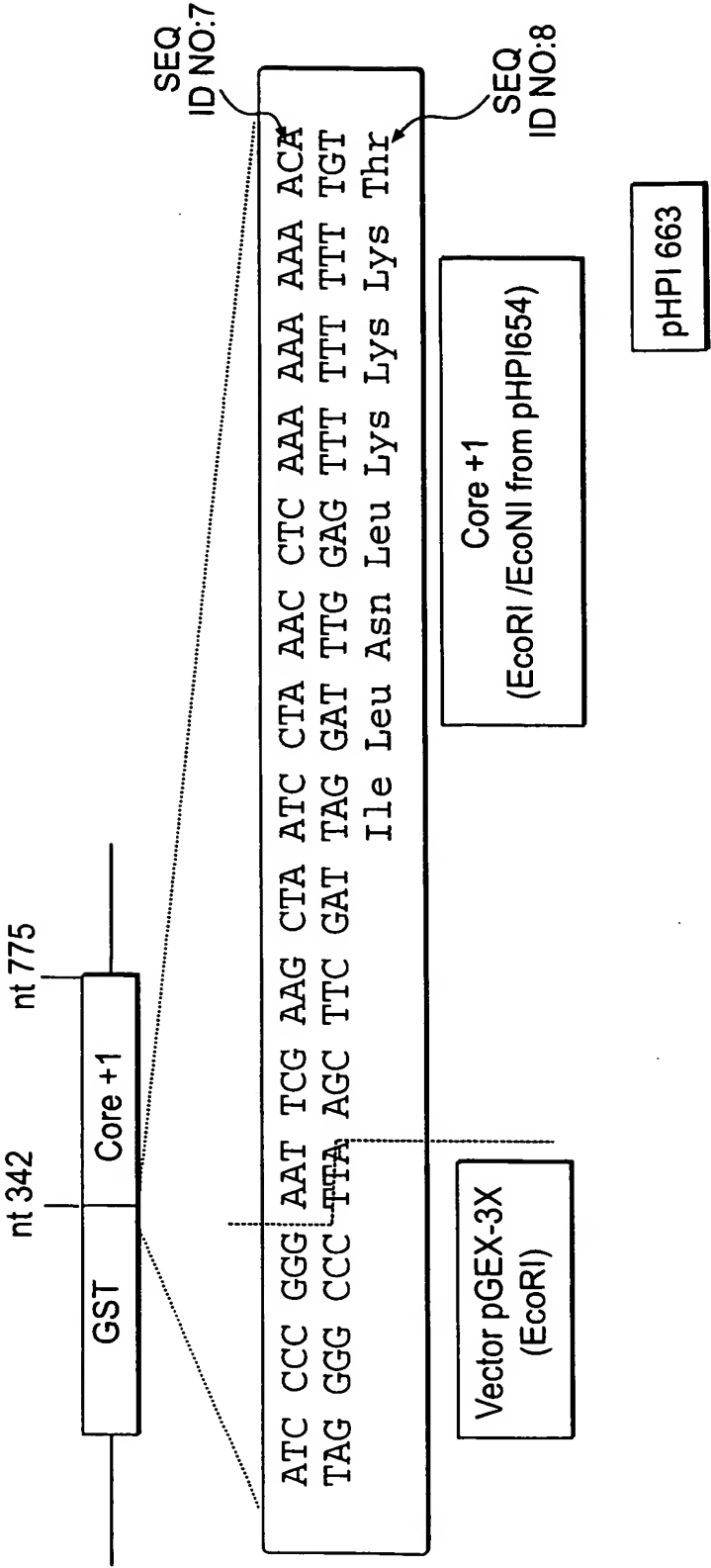


FIG. 4A

GST-CORE+1 RECOMBINANT PROTEINS

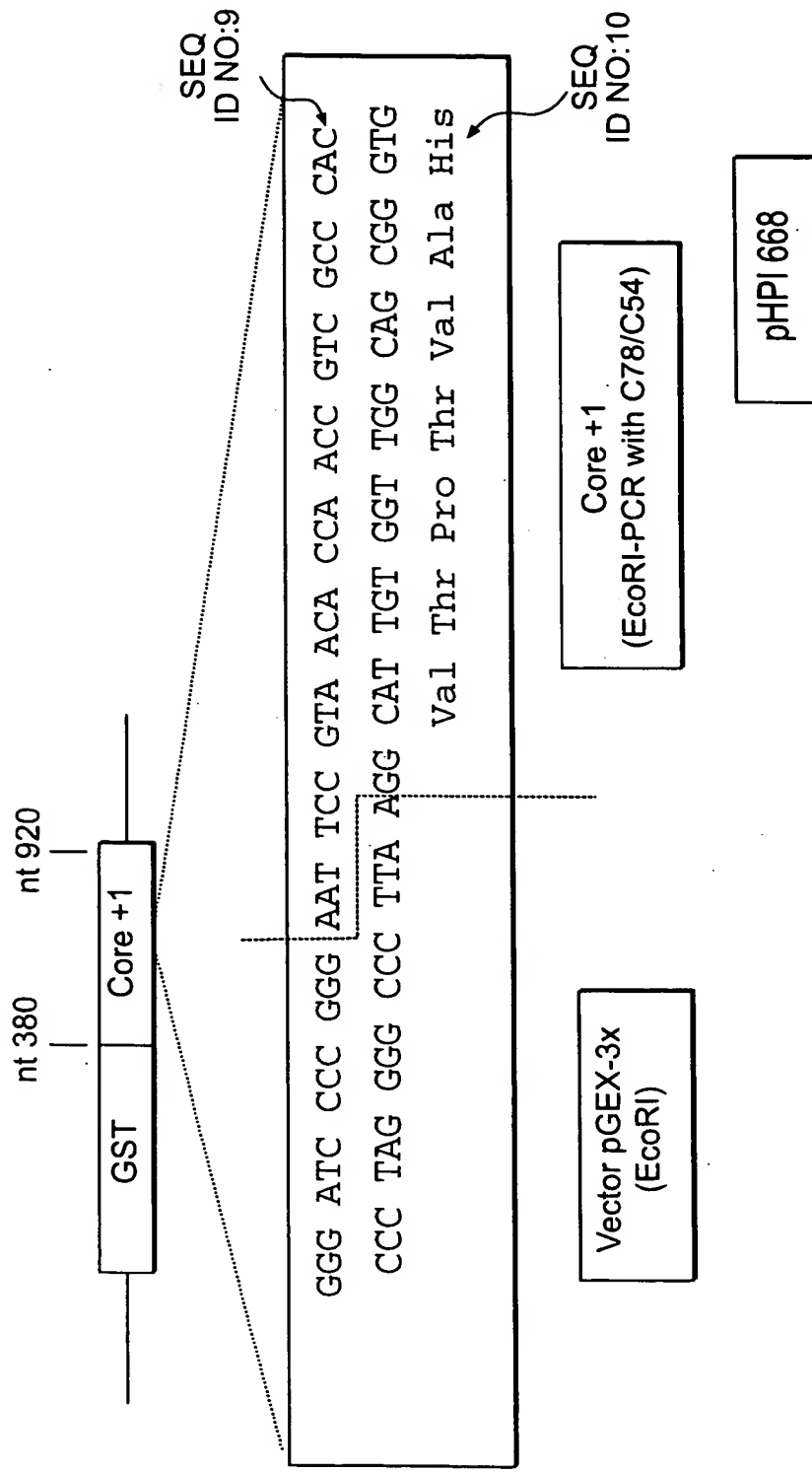


FIG. 4B

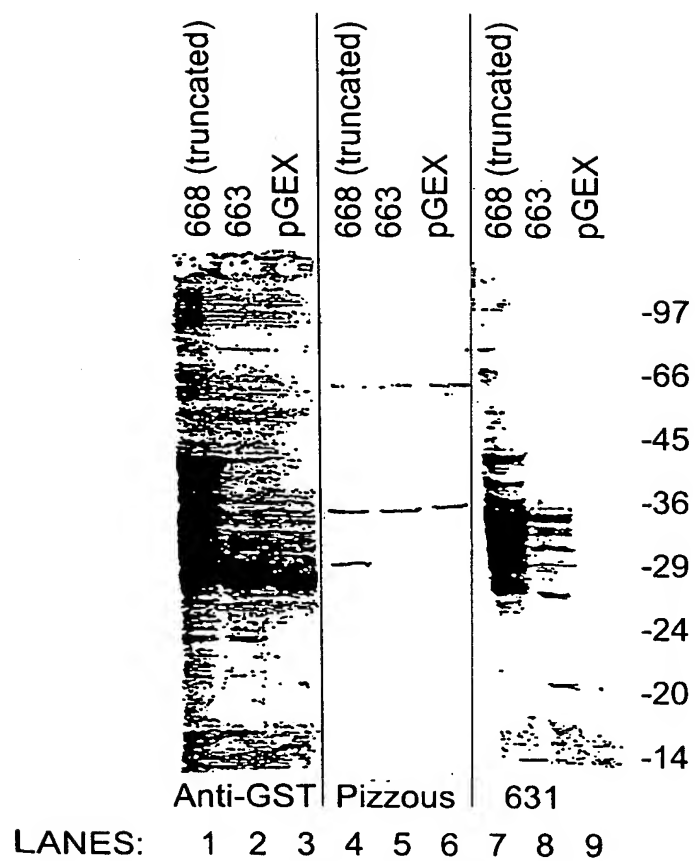


FIG. 5

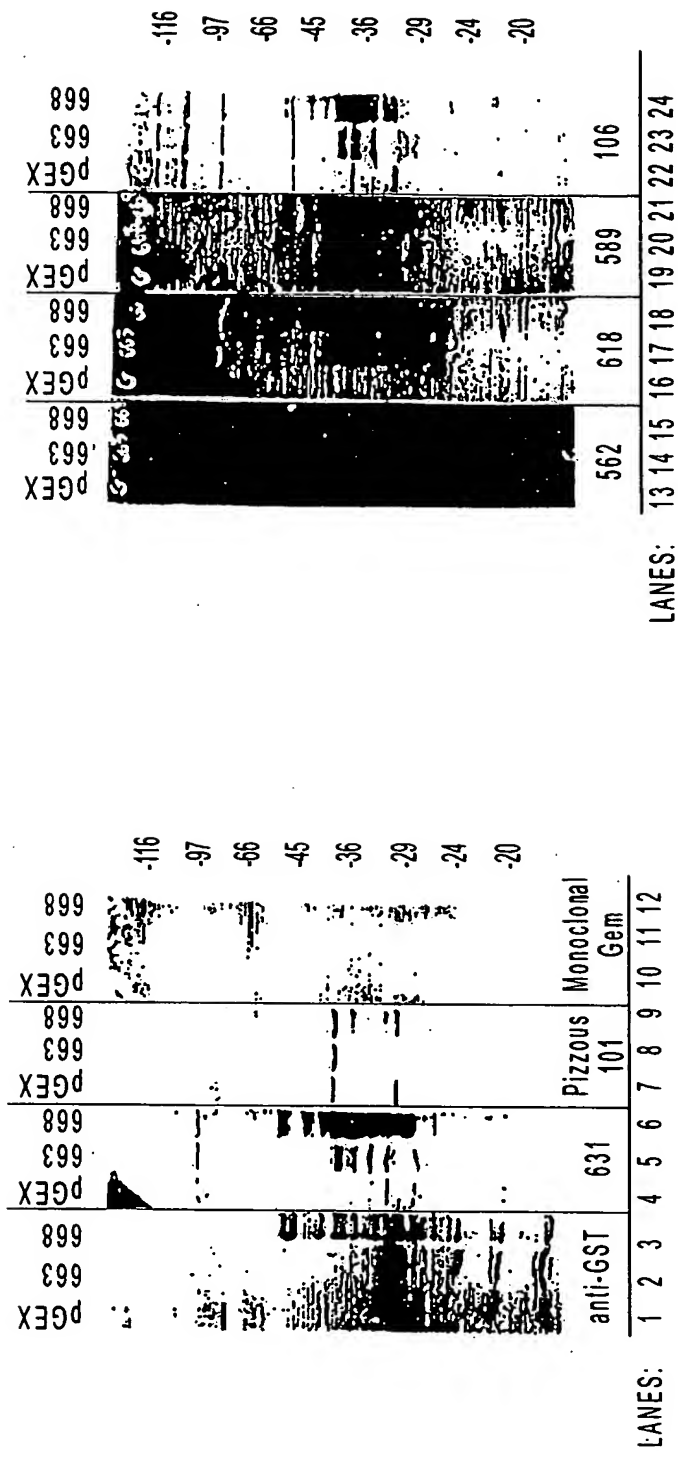


FIG. 6

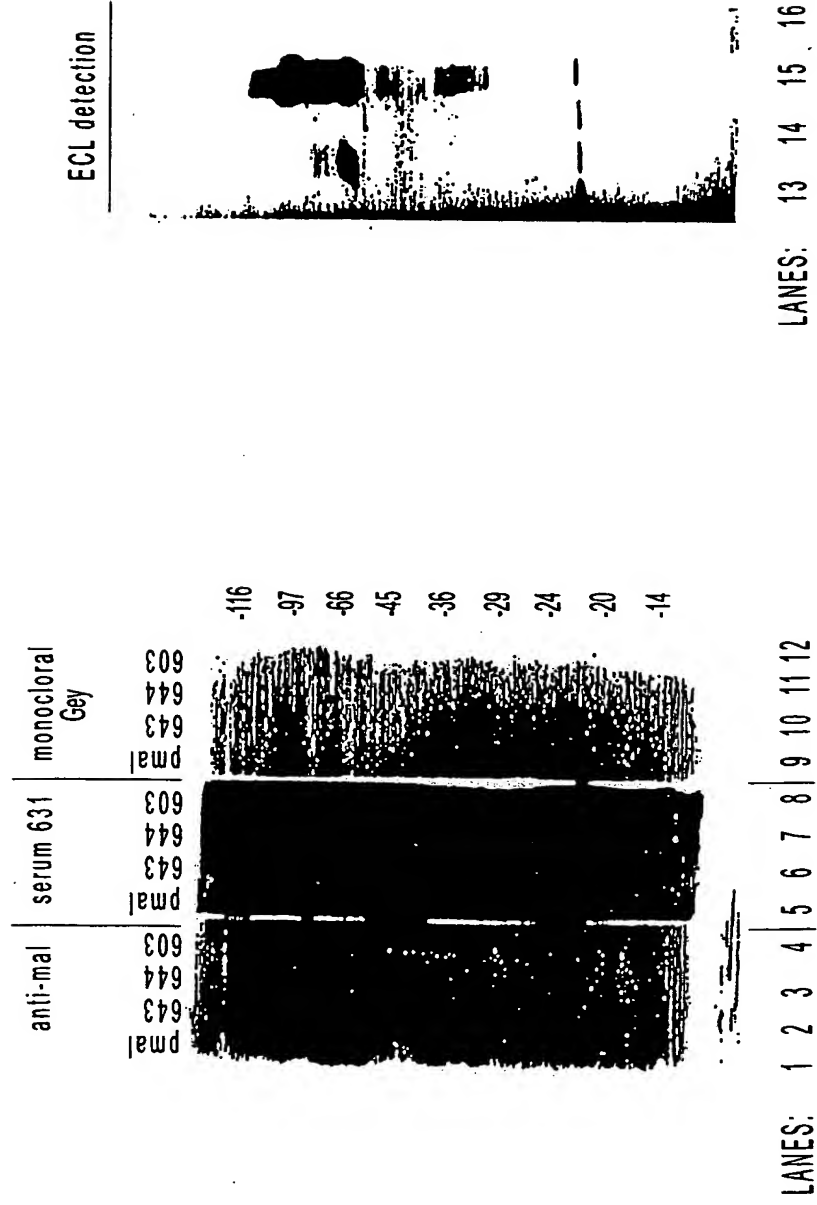


FIG. 7A

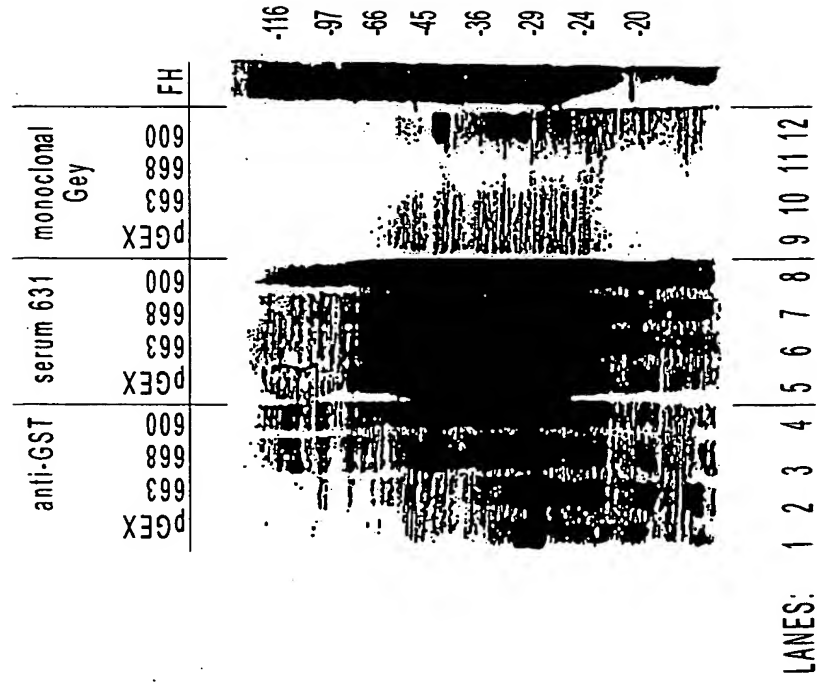


FIG. 7B

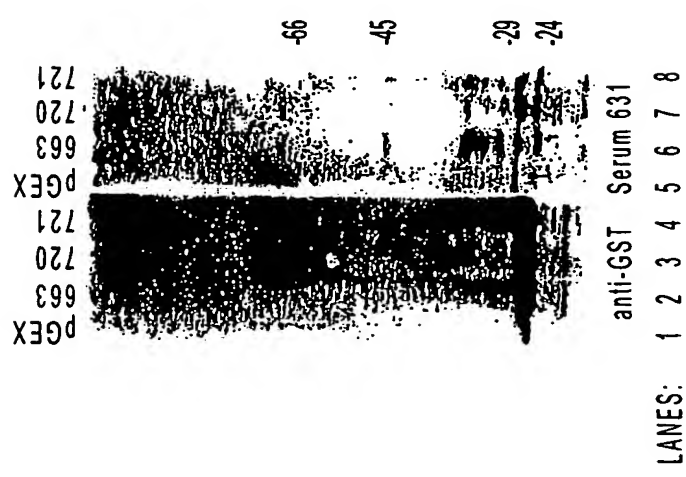
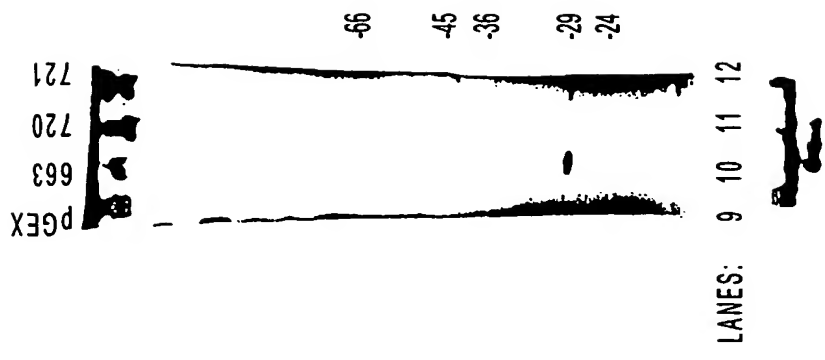


FIG. 8

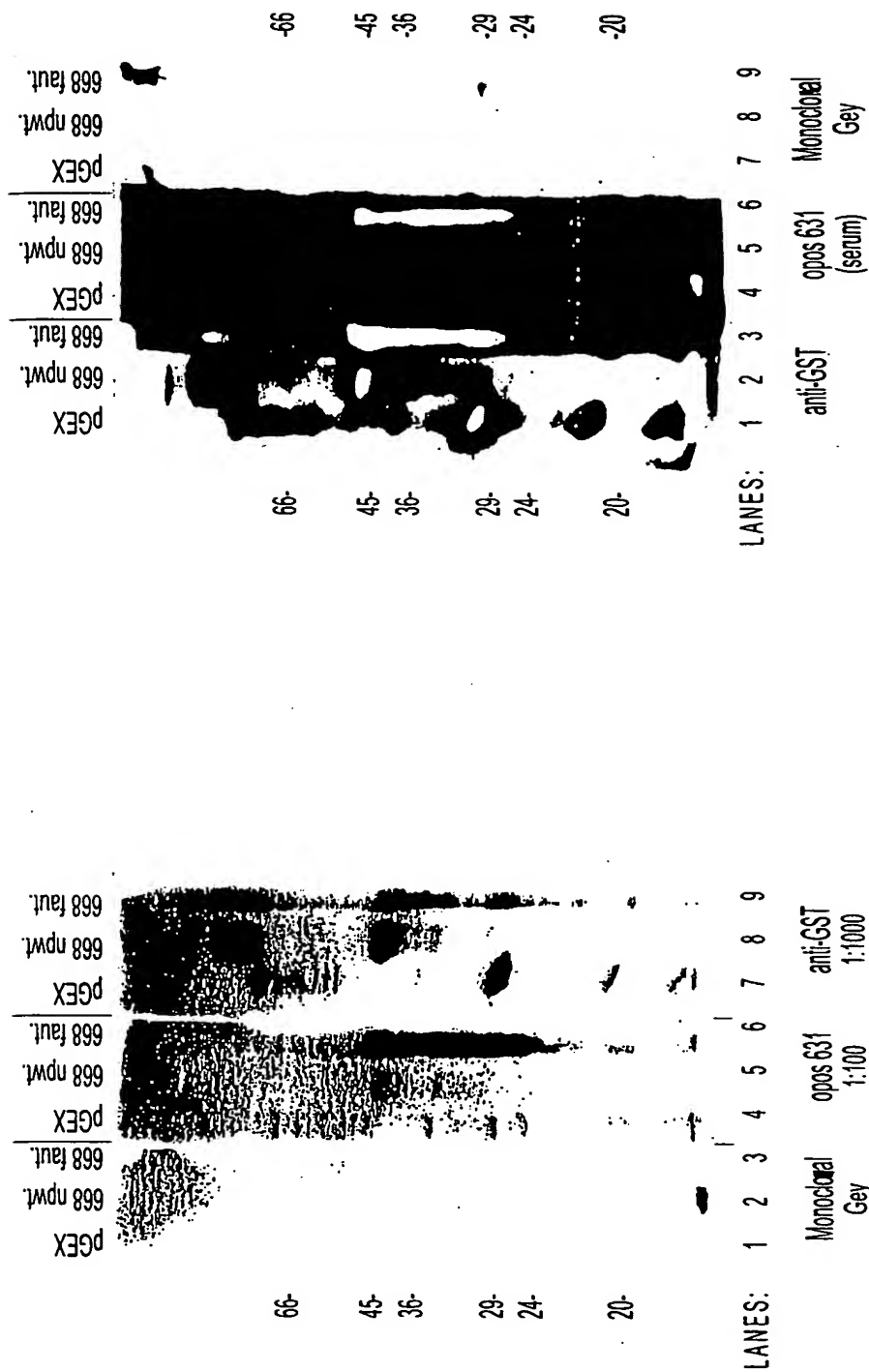


FIG. 9A

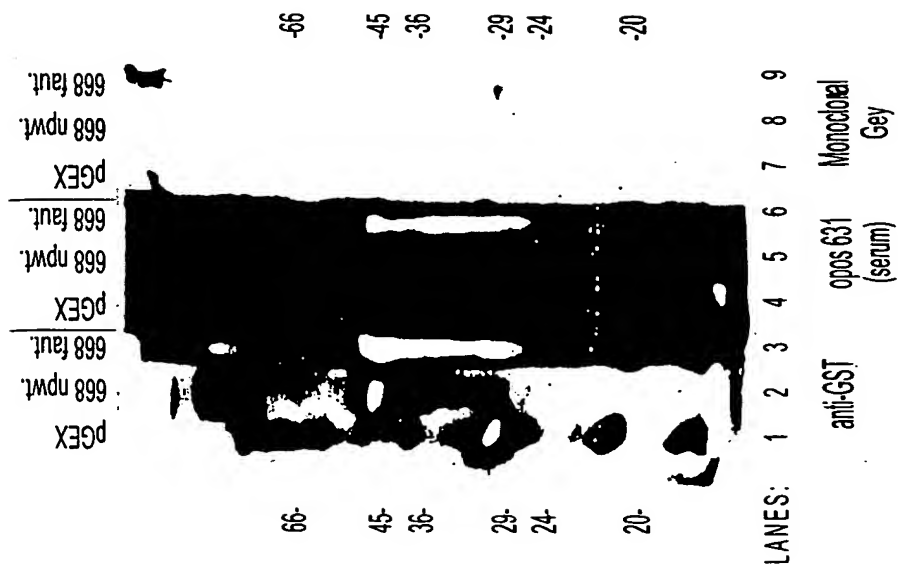


FIG. 9B

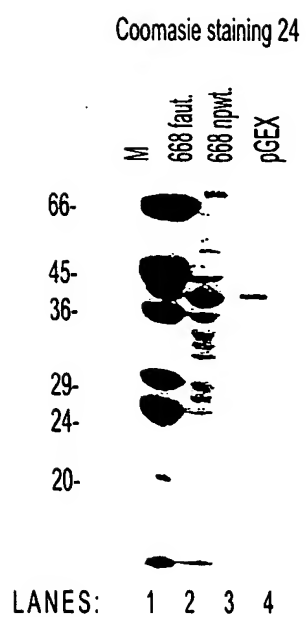
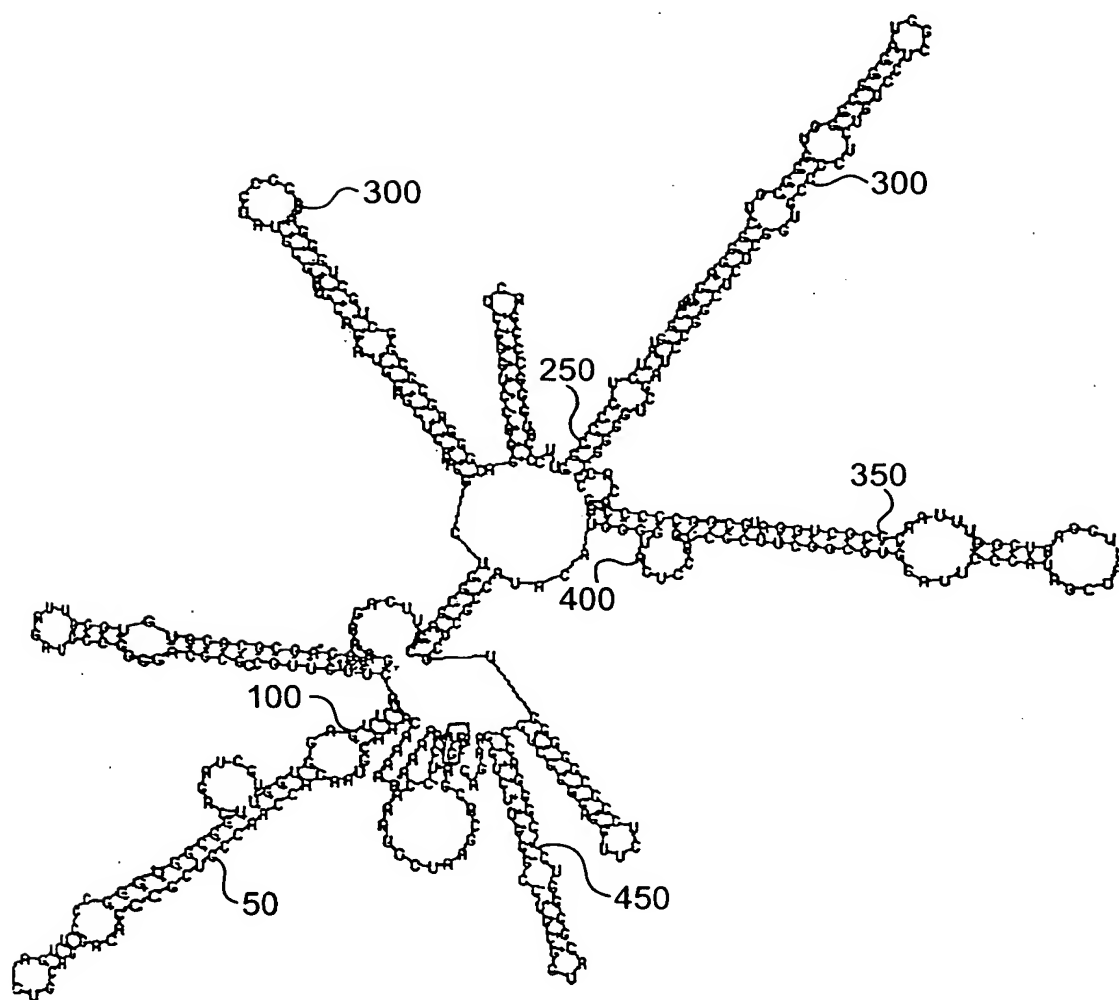


FIG. 9C

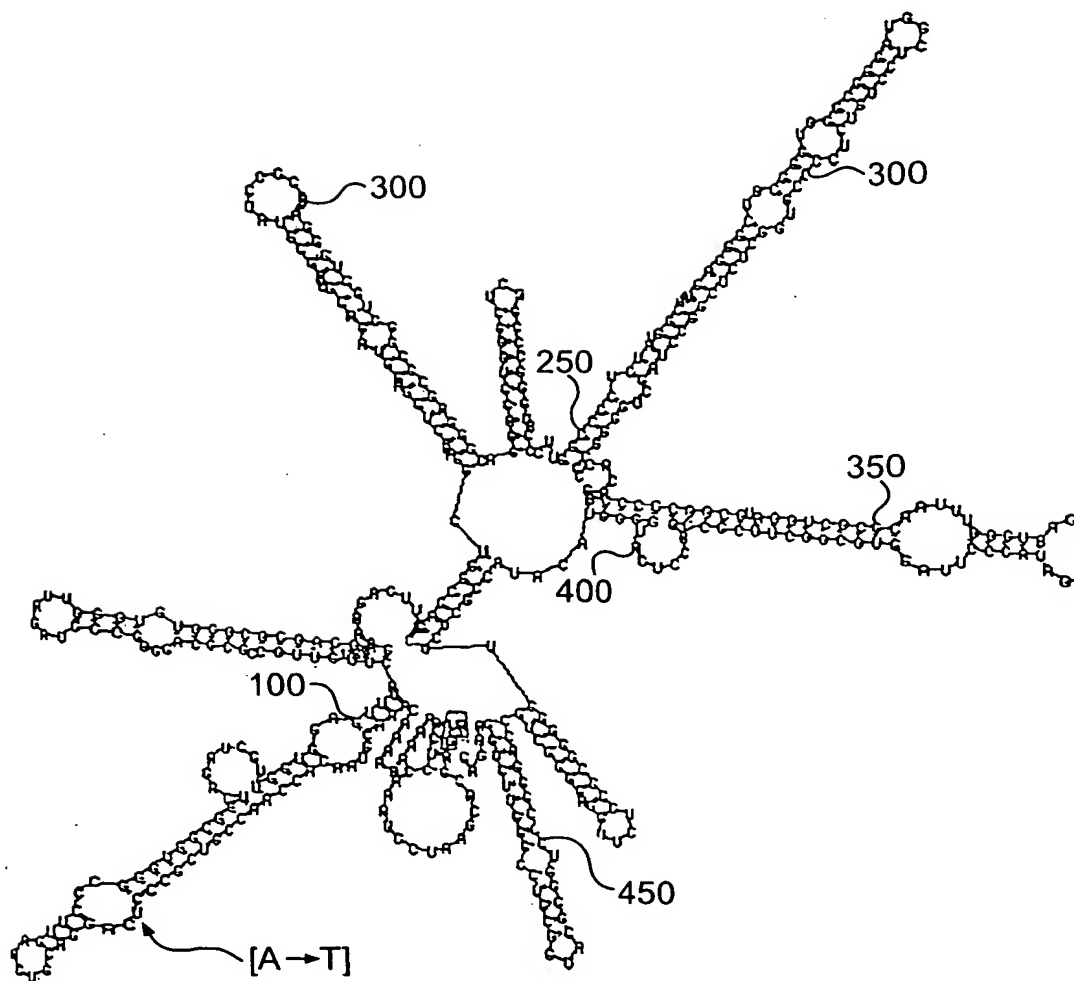
WILD TYPE
pHPI 643 & pHPI 663



(SEQ ID NO: 11)

FIG. 10A

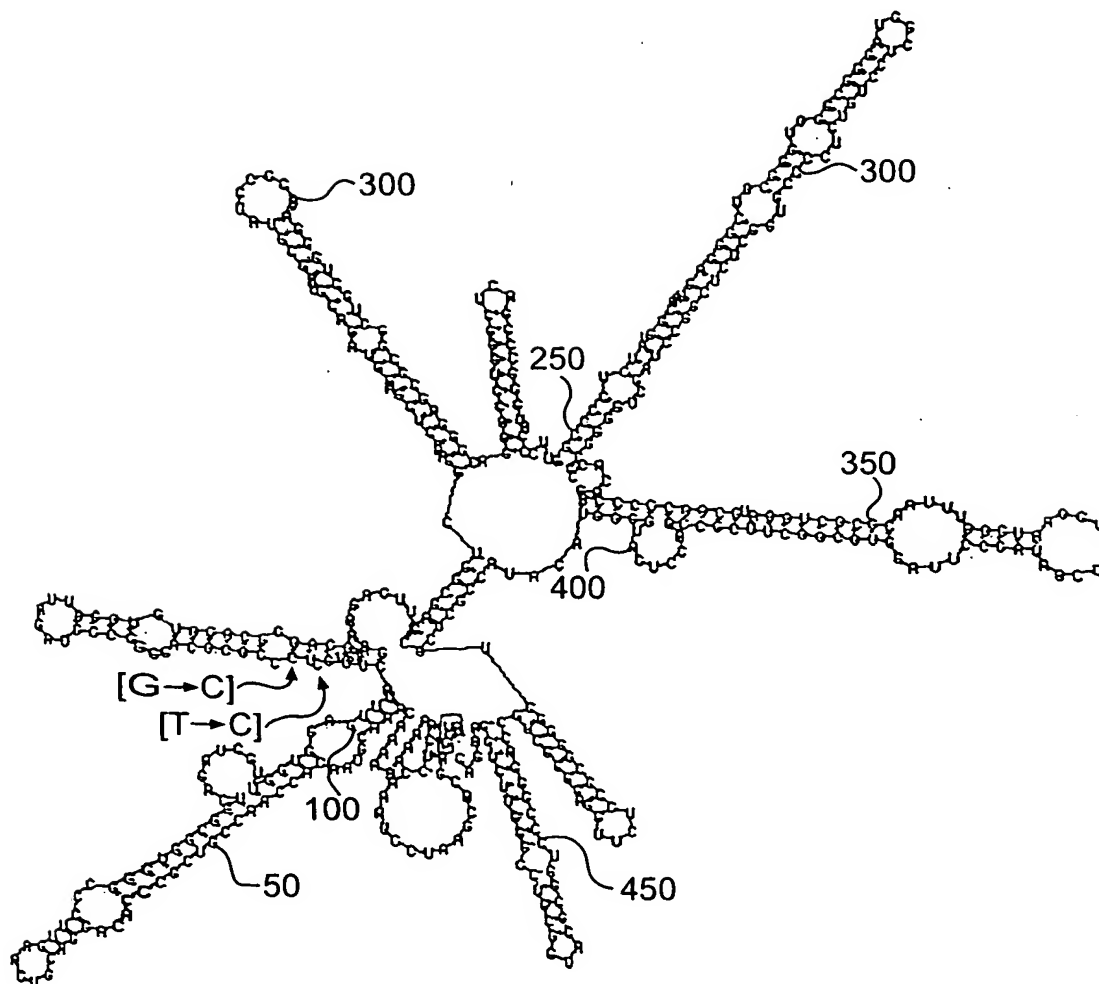
His → Leu
pHPI 676



(SEQ ID NO: 12)

FIG. 10B

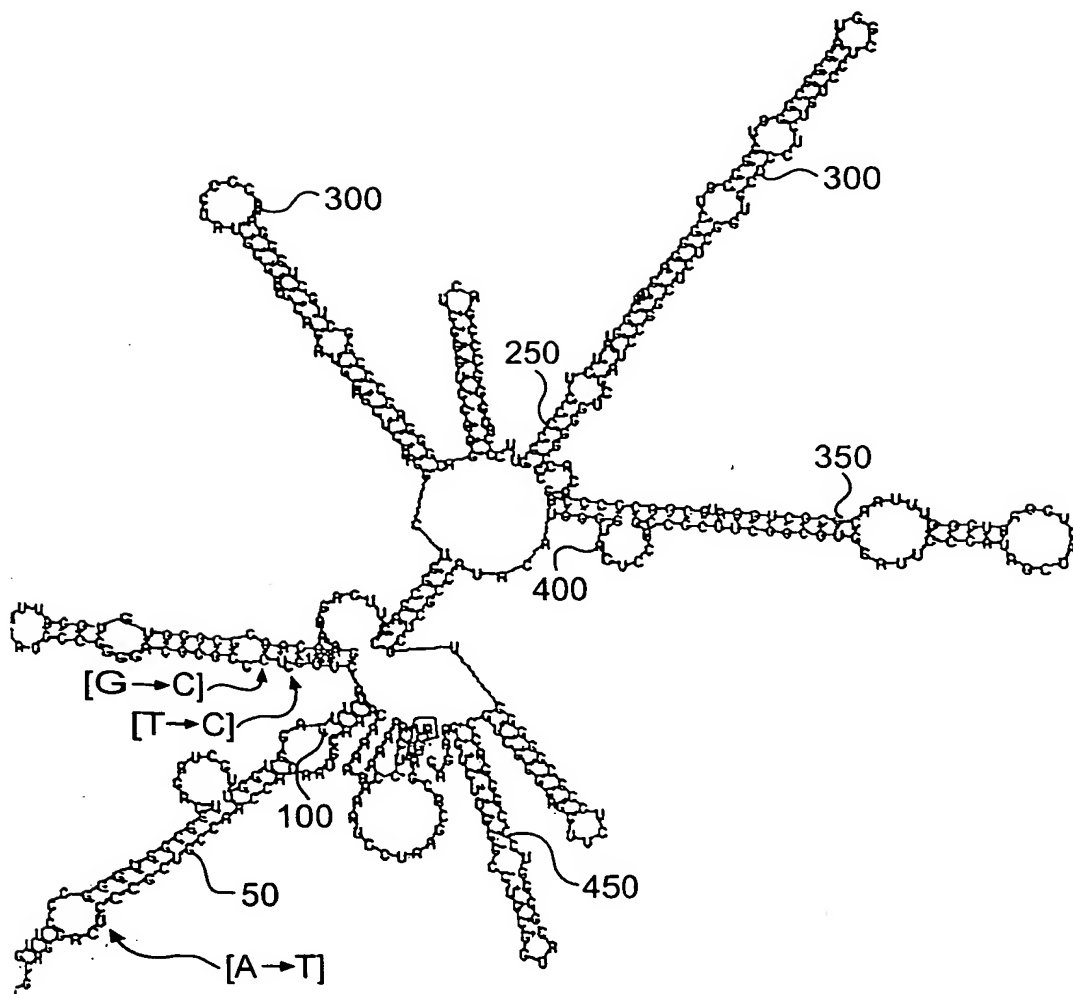
Cys → Ser
pHPI 679



(SEQ ID NO: 13)

FIG. 10C

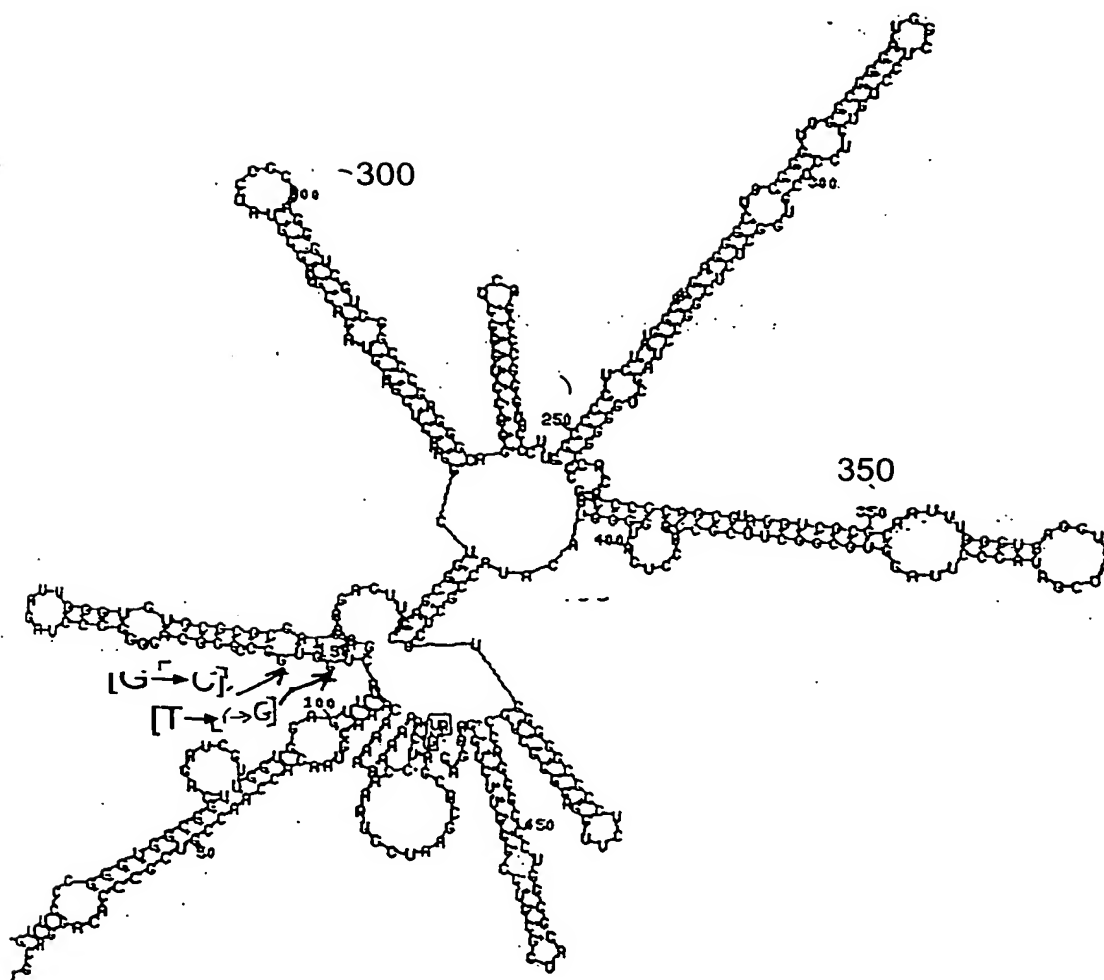
His → Leu & Cys → Ser
pHPI 719



(SEQ ID NO: 14)

FIG. 10D

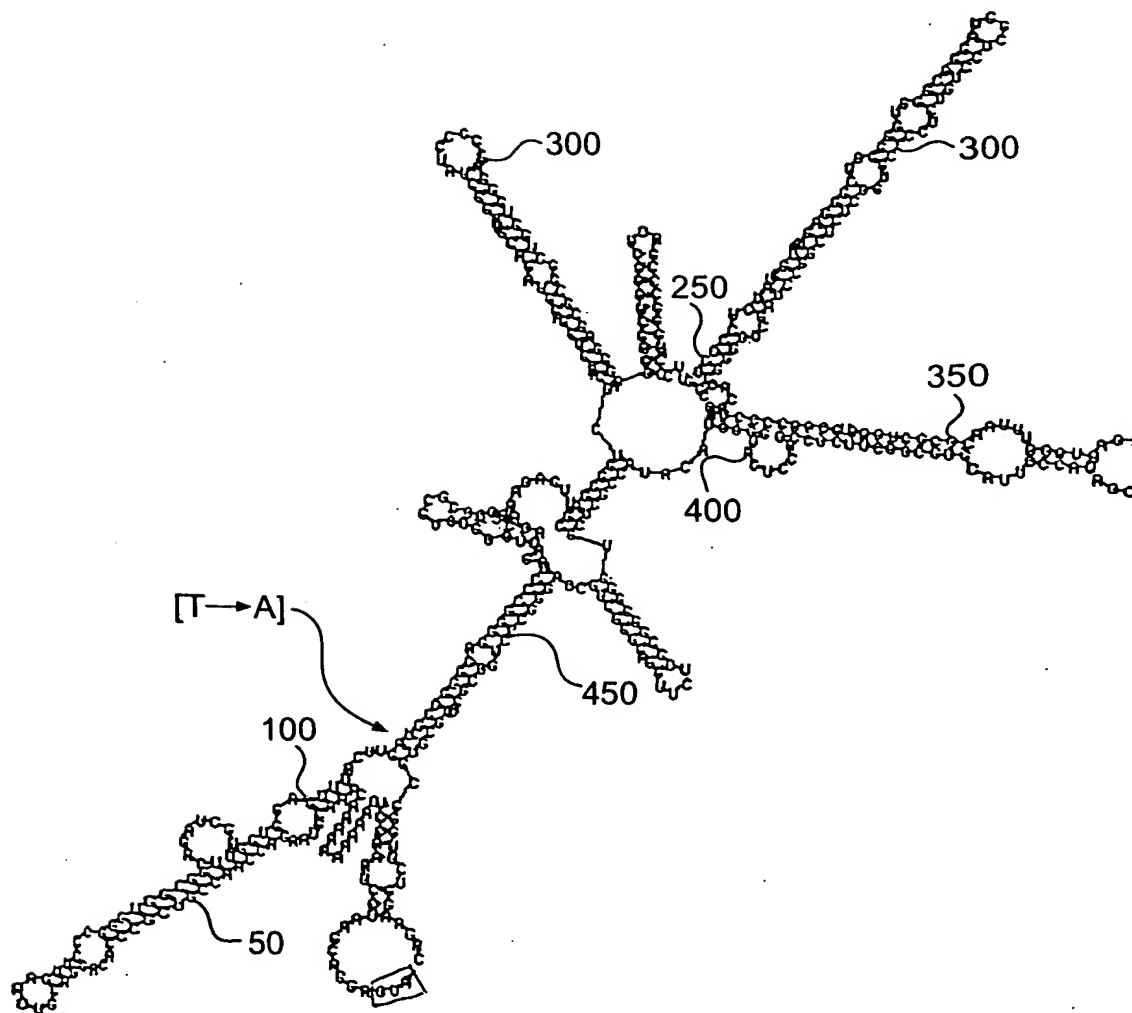
Cys-Cys → Gly- Gly
pHPI 720



(SEQ ID NO: 15)

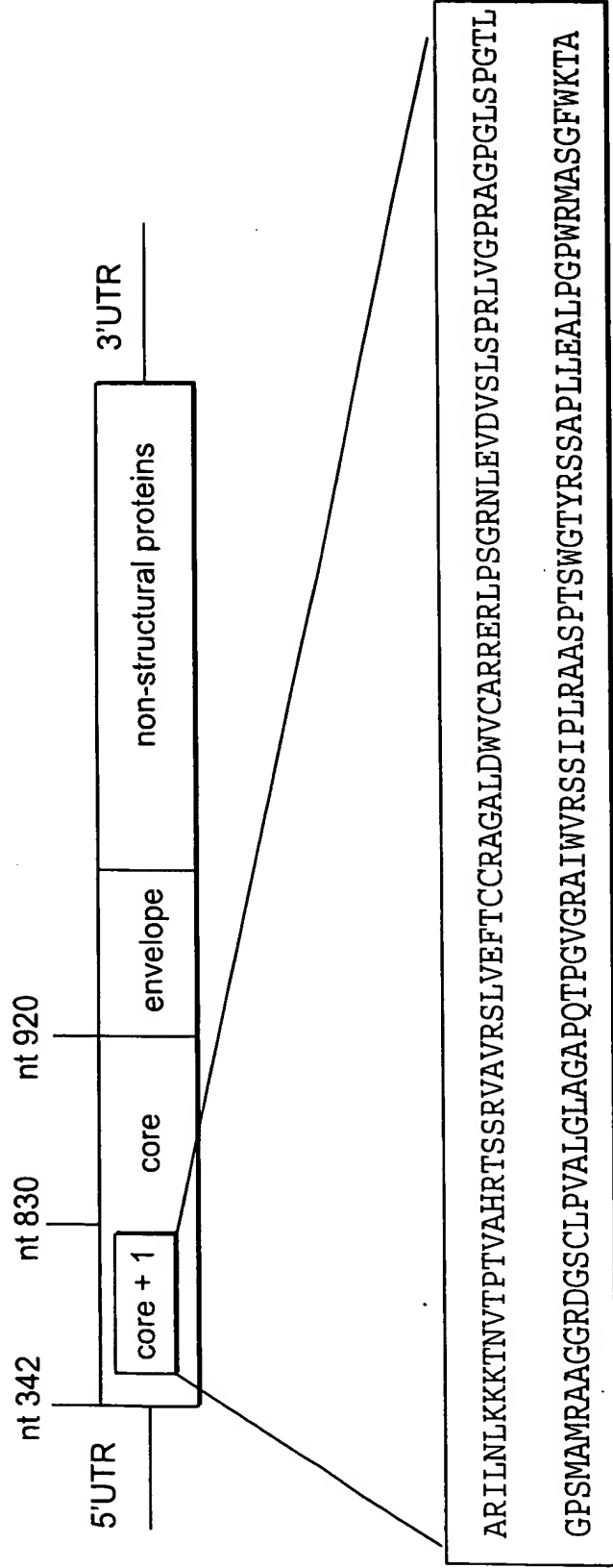
FIG. 10E

Cys → STOP CODON
pHPI 721



(SEQ ID NO: 16)

FIG. 10F



(amino acids 1 to 161 of SEQ ID NO:1)

FIG. 11

SEQUENCE RANGE: 342 TO 840

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350      *      *      *      *      *      *      *      *      *      *      *      *      *      *      *      *
      TGA GCA CGA ATC CTA AAC CTC AAA AAA AAA ACA AAC GTA ACA CCA ACC
      ACT CGT GCT TAG GAT TTG GAG TTT TTT TTT TGT TGT CAT TGT GGT TGG
      *** Ala Arg Ile Leu Asn Leu Lys Lys Lys Thr Asn Val Thr Pro Thr>
      a _ a _ _ _ TRANSLATION OF HCVSEND.SEQ (RITSA) [A] _ a _ a _ _ >

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      PUTATIVE
      SLIPPERY SIGNAL
      400      410      420      430
      *      *      *      *      *      *      *      *
      GTC GCC CAC AGG ACG TCA AGT TCC CGG GTG GCG GTC AGA TCG TTG GTG
      CAG CGG GTG TCC TGC AGT TCA AGG GCC CAC CGC CAG TCT AGC AAC CAC
      Val Ala His Arg Thr Ser Ser Arg Val Ala Val Arg Ser Leu Val>
      a _ a _ _ _ TRANSLATION OF HCVSEND.SEQ (RITSA) [A] _ a _ a _ _ >

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440      *      *      *      *      *      *      *      *      *      *      *      *      *      *      *      *
      GAG TTT ACT TGT TGC CGC GCA GGG GCC CTA GAT TGG GTG TGC GCG CGA
      CTC AAA TGA ACA ACG GCG CGT CCC CGG GAT CTA ACC CAC ACG CGC GCT
      Glu Phe Thr Cys Cys Arg Ala Gly Ala Leu Asp Trp Val Cys Ala Arg>
      a _ a _ _ _ TRANSLATION OF HCVSEND.SEQ (RITSA) [A] _ a _ a _ a _ _ >

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FIG. 12A

490	500	510	520	530
CGA GAA AGA	CTT CCG AGC	GGT CGC AAC	CTC GAG GTA	GAC GTC AGC CTA
GCT CTT TCT	GAA GGC TCG	CCA GCG TTG	GAG CTC CAT	CTG CAG TCG GAT
Arg Glu Arg	Leu Pro Ser	Gly Arg Asn	Leu Glu Val	Asp Val Ser Leu>
a a	a	TRANSLATION OF HCVSEND.SEQ (RITSA)	[A] a a	a a

	540	550	560	570	580
*	*	*	*	*	*
TCC CCA AGG CTC GTC GGC CCG AGG GCA GGA CCT GGG CTC AGC CCG GGT					
AGG GGT TCC GAG CAG CCG GGC TCC CGT CCT GGA CCC GAG TCG GGC CCA					
Ser Pro Arg Leu Val Gly Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly>					
a a TRANSLATION OF HCVSEND.SEQ (RITSA) [A] a a >					

590	600	610	620	630
* * *	* * *	* * *	* * *	* * *
ACC CTT GGC	CCC TCT ATG GCA ATG AGG GCT GCG GGT GGG GAT GGC			
TGG GAA CCG	GGG AGA TAC CGT TAC TCC CGA CGC CCA CCC GCC CTA CCG			
Thr Leu Gly	Pro Ser Met Ala Met Arg Ala Ala Gly Gly Arg Asp Gly			
a a	TRANSLATION OF HCVSEND.SEQ (RITSA) [A] a a a >			

FIG. 12B

10	20	30	40	50	60
* * *	* * *	* * *	* * *	* * *	* * *
*ARILNLKKK	TNVTPTVAHR	TSSSRVAVRS	LVEFTCCRAG	ALDWVCARRE	RLPSGRNLEV
70	80	90	100	110	120
* * *	* * *	* * *	* * *	* * *	* * *
DVLSPLRVG	PRAGPGLSPG	TLGPSMAMRA	AGGRDGSCLP	VALGLAGAPQ	TPGVGRAIWN
130	140	150	160		
* * *	* * *	* * *	* * *		
RSSIPLRAAS	PTSWGTYRSS	APLLEALPGP	WRMASGFWKT	A*TMQQ	

FIG. 13